

- 89 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT:

- (A) NAME: ZENECA LIMITED
(B) STREET: 15 STANHOPE GATE
(C) CITY: LONDON
(E) COUNTRY: UNITED KINGDOM
(F) POSTAL CODE (ZIP): W1Y 6LN
(G) TELEPHONE: 0171 304 5000
(H) TELEFAX: 0171 304 5151
(I) TELEX: 0171 834 2042

10

(ii) TITLE OF INVENTION: PROTEINS

(iii) NUMBER OF SEQUENCES: 131

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

25

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: other nucleic acid

35

- 90 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGAAGCTTGA AGATGGATAC AGTTGGTGCA GC

32

5 (2) INFORMATION FOR SEQ ID NO: 2:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGAAGCTTAG ACAGATGGGG GTGTCGTTTT G

31

25 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

30

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35

- 91 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

Tyr Met

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GACATTCAGC TGACCCAGTC TCCA

24

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- 92 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GACATTGAGC TCACCCAGTC TCCA

24

5 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

20 AGGTSMARCT GCAGSAGTCW GG

22

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- 93 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ACTAGTGGA TTCAGTGTGA GGTSCARCTG CAGCARTCWG G

41

5 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

20 GACATTGAGC TCACCCAGTC TCCAGCAATC ATGTCTGCAT CTCCAGGGGA GAAGGTCACC 60

ATAACCTGCA GTGCCAGCTC AAGTGTAAC TACATGCACT GGTTCAGCA GAAGCCAGGC 120

ACTTCTCCCA AACTCTGGAT TTATAGCACA TCCAACCTGG CTTCTGGAGT CCCTGCTCGC 180

25

TTCAGTGGCA GTGGATCTGG GACCTCTTAC TCTCTCACA TCAGCCGAAT GGAGGCTGAA 240

GATGCTGCCA CTTATTACTG CCAGCAAAGG AGTACTTACC CGCTCACGTT CGGTGCTGGG 300

30 ACCAAGCTGG AGCTGAAACG GGCTGATGCT GCACCAACTG TATCCATCTT CAAGCTT 357

(2) INFORMATION FOR SEQ ID NO: 9:

35

- 94 -

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
 20 25 30

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
 35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala
 100 105

(2) INFORMATION FOR SEQ ID NO: 10:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs

- 95 -

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAGGTGCAGC TGCAGCARTC WGGGGCAGAG CTTGTGAGGT CAGGGGCCTC AGTCAAGTTG 60
TCCTGCACAG CTTCTGGCTT CAACATTAAA GACAACTATA TGCACTGGGT GAAGCAGAGG 120
CCTGAACAGG GCCTGGAGTG GATTGCATGG ATTGATCCTG AGAATGGTGA TACTGAATAT 180
GCCCCGAAGT TCCGGGGCAA GGCCACTTTG ACTGCAGACT CATCCTCCAA CACAGCCTAC 240
CTGCACCTCA GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTACTGTCA TGTCCTGATC 300
TATGCTGGTT ATTTGGCTAT GGACTACTGG GGTCAAGGAA CCTCAGTCGC CGTCTCCTCA 360

25 (2) INFORMATION FOR SEQ ID NO: 11:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 96 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Ala

1 5 10 15

5

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn

20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

10 35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe

50 55 60

15

Arg Gly Lys Ala Thr Leu Thr Ala Asp Ser Ser Ser Asn Thr Ala Tyr

65 70 75 80

Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys

20 85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln

100 105 110

25

Gly Thr Ser Val Ala Val Ser Ser

115 120

(2) INFORMATION FOR SEQ ID NO: 12:

30

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(11) MOLECULE TYPE: other nucleic acid

- 97 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AAGCTTTCCC GCGGGGACAT TGAGCTCACC CAGTCTCCA

39

5 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

20 AAGCTTCTCG AGCTTGGTCC CAGCACCGAA

30

(2) INFORMATION FOR SEQ ID NO: 14:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

- 98 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AAGCTTGGA TTCAGTGTGA GGTGCAGCTG CAGCAG

36

5 (2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

20 AAGCTTCGAG CTCACGGCGA CTGAGGTTCC TTG

33

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid

35

- 99 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

5 CGCGGGGACA TTGAGCTCAC CCAGTCTCCA GCAATCATGT CTGCATCTCC AGGGGAGAAG 120

GTCACCATAA CCTGCAGTGC CAGCTCAAGT GTAACCTTACA TGCACTGGTT CCAGCAGAAG 180

CCAGGCACTT CTCCCAAAT CTGGATTTAT AGCACATCCA ACCTGGCTTC TGGAGTCCCT 240

10 GCTCGCTTCA GTGGCAGTGG ATCTGGGACC TCTTACTCTC TCACAATCAG CCGAATGGAG 300

GCTGAAGATG CTGCCACTTA TTACTGCCAG CAAAGGAGTA CTTACCCGCT CACGTTCCGT 360

15 GCTGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

CCATCTGATG AGCAGTTGAA ATCTGGAAT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

20 CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

25 GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 17:

(1) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

- 100 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

5	Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
	1 5 10 15
10	Val Ile Met Ser Arg Gly Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile
	20 25 30
15	Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser
	35 40 45
20	Ser Ser Val Thr Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser
	50 55 60
25	Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
	65 70 75 80
30	Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
	85 90 95
35	Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg
	100 105 110
	Ser Thr Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
	115 120 125
	Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
	130 135 140
	Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
	145 150 155 160
	Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
	165 170 175
	Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
	180 185 190

- 101 -

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
5 210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

10 (2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 765 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

25 ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60

GTGCAGCTGC AGCARTCAGG GGCAGAGCTT GTGAGGTCAG GGGCCTCACT CAAGTTGTCC 120

TGCACAGCTT CTGGCTTCAA CATTAAAGAC AACTATATGC ACTGGGTGAA GCAGAGGCCT 180

30

GAACAGGGCC TGGAGTGGAT TGCATGGATT GATCCTGAGA ATGGTGATAC TGAATATGCC 240

CCGAAGTTCC GGGGCAAGGC CACTTTGACT GCAGACTCAT CCTCCAACAC AGCCTACCTG 300

35 CACCTCAGCA GCCTGACATC TGAGGACACT GCCGTCTATT ACTGTCATGT CCTGATCTAT 360

GCTGGTTATT TGGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCGCCGT GAGCTCGGCT 420

- 102 -

AGCACCAAGG GACCATCGGT CTTCCCCCTG GCCCCCTGCT CCAGGAGCAC CTCCGAGAGC 480

ACAGCCGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540

5 AACTCAGGCG CTCTGACCAG CGGCGTGAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA 600

CTCTACTCCC TCAGCAGCGT CGTGACGGTG CCCTCCAGCA ACTTCGGCAC CCAGACCTAC 660

ACCTGCAACG TAGATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGACAGT TGAGCGCAAA 720

10

TGTTGTGTCG AGTGCCCACC GTGCCCCGCG CCACCTGTGG CCGGC 765

(2) INFORMATION FOR SEQ ID NO: 19:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly

1

5

10

15

30

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg

20

25

30

Ser Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile

35

35

40

45

Lys Asp Asn Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu

50

55

60

- 103 -

Glu Trp Ile Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala
 65 70 75 80

5 Pro Lys Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Ser Ser Ser Asn
 85 90 95

Thr Ala Tyr Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
 100 105 110

10 Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
 115 120 125

Trp Gly Gln Gly Thr Ser Val Ala Val Ser Ser Ala Ser Thr Lys Gly
 15 130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
 145 150 155 160

20 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190

25 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 195 200 205

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
 30 210 215 220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
 225 230 235 240

35 Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
 245 250 255

- 104 -

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

15

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

20

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

25

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

30

Tyr Ile Cys Asn Val Asn His Asn Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

35

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro
115 120

- 105 -

(2) INFORMATION FOR SEQ ID NO: 21:

5

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

20

GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCTT CCTCCAAGAG CACCTCTGGG 60

GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG 120

25 TGGAAGTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180

GGACTCTACT CCCTCAGCAG CGTGGTGACT GTGCCCTCCA GCAGCTTGGG CACCCAGACC 240

TACATCTGCA ACGTGAATCA CAACCCGAGC AACACCAAGG TCGACAAGAA AGTTGAGCCC 300

30

AAATCTTGTG ACAAGACGCA CACGTGCCCC CCGTGCCCGG CTCCGGAAGT GCTGGGTGGC 360

CCGTAATAG 369

35 (2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids

- 106 -

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

20

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

25

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65 70 75 80

30

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
100 105 110

35

Pro Val Ala Gly
115

- 107 -

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

10

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

15

GCTAGCACCA AGGGACCATC GGTCTTCCCC CTGGCCCCCT GCTCCAGGAG CACCTCCGAG 60

AGCACAGCCG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 120

20 TGGAACTCAG GCGCTCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180

GGACTCTACT CCCTCAGCAG CGTCGTGACG GTGCCCTCCA GCAACTTCGG CACCCAGACC 240

TACACCTGCA ACGTAGATCA CAAGCCCAGC AACACCAAGG TGGACAAGAC AGTTGAGCGC 300

25

AAATGTTGTG TCGAGTGCCC ACCGTGCCCC GCGCCACCTG TGGCCGGC 348

(2) INFORMATION FOR SEQ ID NO: 24:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: protein

- 108 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15
 5
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 10 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 15
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 20
 Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
 100 105 110
 Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
 25 115 120 125
 Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
 130 135 140
 30
 Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
 145 150 155 160
 Ala Pro Glu Leu Leu Gly Gly
 165
 35

(2) INFORMATION FOR SEQ ID NO: 25:

(1) SEQUENCE CHARACTERISTICS:

- 109 -

- (A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GCTAGCACCA AGGGCCCATC GGTCTTCCCC CTGGCGCCCT GCTCCAGGAG CACCTCTGGG 60
15 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGG 120
TGGAATCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180
GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 240
20 TACACCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAG AGTGGAGCTG 300
AAAACCCAC TTGGTGACAC AACTCACACG TGCCCTAGGT GTCCTGAACC TAAATCTTGT 360
25 GACACACCTC CCCCCTGCCC ACGGTGCCCA GAGCCCAAAT CTTGCGACAC GCCCCACCG 420
TGTCCTGAT GTCTGAACC AAAGAGCTGT GACTACTCCAC CGCCCTGCCC GAGGTGCCCA 480
GCACCTGAAC TCCTGGGAGG A 501

30

(2) INFORMATION FOR SEQ ID NO: 26:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35

- 110 -

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Ser Ala Ser Ser Ser Val Thr Tyr Met His
1 5 10

10 (2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

25 Ser Thr Ser Asn Leu Ala Ser
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

- 111 -

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

5 Gln Gln Arg Ser Thr Tyr Pro Leu Thr
 1 5

(2) INFORMATION FOR SEQ ID NO: 29:

10

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

25 (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

 Asp Asn Tyr Met His
 1 5

30 (2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 112 -

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Phe Asn Ile Lys Asp Asn Tyr Met His

1

5

10 (2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe Arg

1

5

10

15

Gly

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- 113 -

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
1 5 10

10

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

25

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 34:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

- 114 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TCGAGAGATC TAAGCTTCCG CGGGAATTCC TCGAGGAGCT CCCCGGGGGA TCCGTCGACT 60

5

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

20

CTAGAGTCGA CGGATCCCCC GGGGAGCTCC TCGAGGAATT CCCGCGGAAG CTTAGATCTC 60

(2) INFORMATION FOR SEQ ID NO: 36:

25

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

- 115 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

AAGCTTCCCG GGTATTAAAG CAGAACTTG

29

5 (2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

20 ACTAGTGGAT CCCAGACATG ATAAGATAC

29

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GGTCTATATA AGCAGAGCTG TCTGGCTAAC TAGAGAACC

39

- 116 -

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GGTTCTCTAG TTAGCCAGAC AGCTCTGCTT ATATAGACC

39

15 (2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

30 GGACTTTCCT ACTTGGCAG

19

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 117 -

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GGCAACTAGA AGGCACAGTC

20

10

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

25

AGCTTGCCGC CACCATGGAT TTTCAAGTGC AGATTTTCAG CTCCTGCTA ATCAGTGCTT

60

CAGTCATAAT GTCCCGC

77

30 (2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

- 118 -

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GGGACATTAT GACTGAAGCA CTGATTAGCA GGAAGCTGAA AATCTGCACT TGAAAATCCA 60

TGGTGGCGGC A 71

10

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

25

AGCTTGCCGC CACCATGAAG TTGTGGCTGA ACTGGATTTT CCTTGTAACA CTTTAAATG 60

G 61

30 (2) INFORMATION FOR SEQ ID NO: 45:

(1) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- 119 -

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

AATTCCATTT AAAAGTGTTA CAAGGAAAAT CCAAGTTCAGC CACAACTTCA TGGTGGCGGC 60

A 61

10

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

AAGCTTCTCG AGATCAAACG GACTGTGGCT GCACCATCTG TCTTCATCTT CCCGCCATCT 60

GATGAGCAGT TGAAATCTGG AACTGCCTCT GTTGTGTGCC TGCTGAATAA CTTCTATCCC 120

30 AGAGAGGCCA AAGTACAGTG GAAGGTGGAT AACGCCCTCC AATCGGGTAA CTCCCAGGAG 180

AGTGTCAAG AGCAGGACAG CAAGGACAGC ACCTACAGCC TCAGCAGCAC CCTGACGCTG 240

AGCAAAGCAG ACTACGAGAA ACACAAAGTC TACGCCTGCG AAGTACCCA TCAGGGCCTG 300

AGTTCGCCCC TCACAAAGAG CTTCAACAGG GGAGAGTGTT AATAGCCCGG GACTAGT 357

(2) INFORMATION FOR SEQ ID NO: 47:

- 120 -

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

10

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

15 GGAAGCTTGA GCTCGGCTAG CACCAAGGGA CCATCGGTCT TCCCCCTGGC CCCCTGCTCC 60
AGGAGCACCT CCGAGAGCAC AGCCGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA 120
CCGGTGACGG TGTCGTGGAA CTCAGGCGCT CTGACCAGCG GCGTGACAC CTTCCCGGCT 180
20 GTCCTACAGT CCTCAGGACT CTA CTCCCTC AGCAGCGTCG TGACGGTGCC CTCCAGCAAC 240
TTCGGCACCC AGACCTACAC CTGCAACGTA GATCACAAGC CCAGCAACAC CAAGGTGGAC 300
25 AAGACAGTTG AGCGCAAATG TTGTGTCGAG TGCCCACCGT GCCCGGCGCC ACCTGTGGCC 360
GGCTAATAGC CCGGGACTAG T 381

(2) INFORMATION FOR SEQ ID NO: 48:

30

(1) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- 121 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

5 AAGCTTTCCC GCGGCGACAT CCAGATGACC CAGAGCCCAA GCAGCCTGAG CGCTAGCGTG 60
GGTGACAGAG TGACCATCAC GTGTAGTGCC AGCTCAAGTG TAACTTACAT GCACTGGTAC 120
CAGCAGAAGC CAGGTAAGGC TCCAAAGCTG CTGATCTACA GCACATCCAA CCTGGCTTCT 180
10 GGTGTGCCAA GCAGATTCTC CGGAAGCGGT AGCGGCACCG ACTACACCTT CACCATCAGC 240
AGCCTCCAGC CAGAGGATAT CGCCACCTAC TACTGCCAGC AGAGGAGTAC TTACCCGCTC 300
ACGTTCCGCC AAGGGACCAA GCTCGAGATC AAACGGACTA GT 342

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

30 GACATCCAGA TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60
ATCACGTGTA GTGCCAGCTC AAGTGTA ACT TACATGCACT GGTACCAGCA GAAGCCAGGT 120
35 AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180
TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240

- 122 -

GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300

ACCAAGCTCG AGATCAAACG G 321

5 (2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

20 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 3025 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 4530 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 8035 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr
85 90 95

- 123 -

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg

100

105

(2) INFORMATION FOR SEQ ID NO: 51:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

15

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

CGCGGCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120

20 GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACCTACA TGCACTGGTA CCAGCAGAAG 180

CCAGGTAAGG CTCCAAAGCT GCTGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240

AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300

25

CCAGAGGATA TCGCCACCTA CTA CTGCCAG CAGAGGAGTA CTTACCCGCT CACGTTCCGGC 360

CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

30 CCATCTGATG AGCAGTTGAA ATCTGGAAC TGCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCCTG 600

35

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

- 124 -

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 235 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

20 Val Ile Met Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
35 40 45

25 Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

30 Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile
85 90 95

35 Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg
100 105 110

- 125 -

Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 115 120 125

5 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 145 150 155 160

10 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 165 170 175

15 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 195 200 205

20 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

25 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35

- 126 -

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GAAGCTTGGA ATTCAGTGTG AGGTGCAGCT GCAGCAGAGC GGTCCAGGTC TCGTACGGCC 60
5 TAGCCAGACC CTGAGCCTCA CGTGACCCGC ATCTGGCTTC AACATTAAGG ACAATTACAT 120
GCACTGGGTG AGACAGCCAC CTGGACGAGG CCTTGAGTGG ATTGGATGGA TTGACCCTGA 180
GAATGGTGAC ACTGAGTACG CACCTAAGTT TCGCGGCCGC GTGACAATGC TGGCAGACAC 240
10 TAGTAAGAAC CAGTTCAGCC TGAGACTCAG CAGCGTGACA GCCGCCGACA CCGCGGTCTA 300
TTATTGTAC GTCCTGATAT ACGCCGGGTA TCTGGCAATG GACTACTGGG GCCAAGGGAC 360
15 CCTCGTCACC GTGAGCTCGA CTAGT 385

(2) INFORMATION FOR SEQ ID NO: 54:

(1) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (11) MOLECULE TYPE: other nucleic acid

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

30 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60
ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120
CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180
35 GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACA CTAGTAAGAA CCAATTTCAGC 240
CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

- 127 -

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

5 (2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

20 Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn

20 25 30

25 Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile

35 40 45

30 Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe

50 55 60

Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser

65 70 75 80

35 Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys

85 90 95

- 128 -

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

5

115

120

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 765 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAAGTGTGAG 60

GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC GTACGGCCTA GCCAGACCCT GAGCCTCAGC 120

25

TGACCCGCAT CTGGCTTCAA CATTAAGGAC AATTACATGC ACTGGGTGAG ACAGCCACCT 180

GGACGAGGCC TTGAGTGGAT TGGATGGATT GACCCTGAGA ATGGTGACAC TGAGTACGCA 240

30

CCTAAGTTTC GCGGCCGCGT GACAATGCTG GCAGACACTA GTAAGAACCA GTTCAGCCTG 300

AGACTCAGCA GCGTGACAGC CGCCGACACC GCGGTCTATT ATTGTCACGT CCTGATATAC 360

GCCGGGTATC TGGCAATGGA CTAAGGGGGC CAAGGGACCC TCGTCACCGT GAGCTCGGCT 420

35

AGCACCAAGG GACCATCGGT CTTCCCCCTG GCCCCCTGCT CCAGGAGCAC CTCCGAGAGC 480

ACAGCCGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540

- 129 -

AACTCAGGCG CTCTGACCAG CGGCGTGAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA 600

CTCTACTCCC TCAGCAGCGT CGTGACGGTG CCCTCCAGCA ACTTCGGCAC CCAGACCTAC 660

5 ACCTGCAACG TAGATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGACAGT TGAGCGCAAA 720

TGTTGTGTGG AGTGCCCACC GTGCCCCGGC CCACCTGTGG CCGGC 765

10 (2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

25 Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly

1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg

20 25 30

30 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile

35 40 45

Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu

35 50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala

65 70 75 80

- 130 -

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn

85

90

95

5 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val

100

105

110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr

115

120

125

10

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly

130

135

140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser

15

145

150

155

160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

165

170

175

20

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

180

185

190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

195

200

205

25

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val

210

215

220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys

30

225

230

235

240

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly

245

250

255

35 (2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

- 131 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GGCGACATCC AGCTGACCCA GAGCCCAAGC AGCCTGAGCG

40

10

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

25

CTAGCGCTCA GGCTGCTTGG GCTCTGGGTC AGCTGGATGT CGCCGC

46

(2) INFORMATION FOR SEQ ID NO: 60:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

- 132 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GACATCCAGC TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60
 5 ATCACGTGTA GTGCCAGCTC AAGTGTAAC TACATGCACT GGTACCAGCA GAAGCCAGGT 120
 AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180
 TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240
 10 GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300
 ACCAAGCTCG AGATCAAACG G 321

15 (2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

30 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
 20 25 30
 35 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45

- 133 -

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

5 Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr
85 90 95

10 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

(2) INFORMATION FOR SEQ ID NO: 62:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: other nucleic acid

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GGCCAGATCG TGCTGACCCA GAGCCCAAGC AGCCTGAGCG

40

30 (2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: other nucleic acid

- 134 -

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CTAGCGCTCA GGCTGCTTGG GCTCTGGGTC AGCAGGATCT GGCCGC

46

(2) INFORMATION FOR SEQ ID NO: 64:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

CAGATCGTGC TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60

25

ATCACGTGTA GTGCCAGCTC AAGTGTAAC TACATGCACT GGTACCAGCA GAAGCCAGGT 120

AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180

30 TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240

GATATCGCCA CCTACTACTG. CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300

ACCAAGCTCG AGATCAAACG G 321

35

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- 135 -

- (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
 20 25 30

20

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

25

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
 65 70 75 80

30

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

35 (2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

- 136 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CGTATTAGTC ATCGCTATTA CC

22

(2) INFORMATION FOR SEQ ID NO: 67:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

20

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GTTGGATGTG CTGTAGATCC ACAGCTTTGG AGCCTTACC

39

(2) INFORMATION FOR SEQ ID NO: 68:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- 137 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

5

TCCGTTTGAT CTCGAGCTTG G

21

(2) INFORMATION FOR SEQ ID NO: 69:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GGTAAGGCTC CAAAGCTGTG GATCTACAGC ACATCCAAC

39

25 (2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

- 138 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GACATCCAGA TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60
 5 ATCACGTGTA GTGCCAGCTC AAGTGTAAC TACATGCACT GGTACCAGCA GAAGCCAGGT 120
 AAGGCTCCAA AGCTGTGGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180
 TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240
 10 GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300
 ACCAAGCTCG AGATCAAACG G 321

15 (2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

30 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
 20 25 30
 35 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
 35 40 45

- 139 -

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
 5 65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr
 85 90 95

10 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO: 72:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: other nucleic acid

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CCTTGAGTGG ATTGCATGGA TTGACCCTGA GAATGGTGAC ACTGAGTACG CACCTAAGTT 60
 30 TCGC 64

(2) INFORMATION FOR SEQ ID NO: 73:

- 35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid

- 140 -

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

10

GGCCGCGAAA CTTAGGTGCG TACTCAGTGT CACCATTCTC AGGGTCAATC CATGCAATCC 60

ACTCAAGG 68

15 (2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

30 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

35

GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACA CTAGTAAGAA CCAGTTCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

- 141 -

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

(2) INFORMATION FOR SEQ ID NO: 75:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

20

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln

1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn

20 25 30

25

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile

35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe

50 55 60

30

Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser

65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys

35

85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln

100 105 110

- 142 -

Gly Thr Leu Val Thr Val Ser Ser

115

120

5 (2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

20 GGCCGCGTGA CAATGCTGGC AGACTCAAGT AAGAACCAGG CCAGCCTGAG ACTCAGCAGC 60

GTGACAGCCG CCGACACCGC 80

(2) INFORMATION FOR SEQ ID NO: 77:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

- 143 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGTGTGGGCG GCTGTCACGC TGCTGAGTCT CAGGCTGGCC TGTTCTTAC TTGAGTCTGC 60

5 CAGCATTGTC ACGC 74

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

25 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

30

GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

35 TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

- 144 -

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Arg Gly Arg Val Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

- 145 -

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: other nucleic acid

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60
ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120
20 CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180
GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240
25 CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300
TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

30 (2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

1 5 10 15

20 25 30

35 40 45

50 55 60

65 70 75 80

20

100 105 110

115 120

30

35

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: other nucleic acid

- 147 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

5

GGCCGCGCCA CAATGCTGGC AGACACTAGT AAGAACCAGT TCAGCCTGAG ACTCAGCAGC 60

GTGACAGCCG CCGACACCGC 80

10 (2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

25 GGTGTCGGCG GCTGTCACGC TGCTGAGTCT CAGGCTGAAC TGGTTCTTAC TAGTGTCTGC 60

CAGCATTGTG GCGC 74

(2) INFORMATION FOR SEQ ID NO: 84:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- 148 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

5 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60
 ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120
 CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180
 10 GCACCTAAGT TTCGCGGCCG CGCCACAATG CTGGCAGACA CTAGTAAGAA CCAGTTCAGC 240
 CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300
 TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360
 15

(2) INFORMATION FOR SEQ ID NO: 85:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
 1 5 10 15

35 Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
 20 25 30

- 149 -

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
 35 40 45

5 Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
 50 55 60

Arg Gly Arg Ala Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

10 Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

15 His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 86:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

25

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

35 GGCCGCGCCA CAATGCTGGC AGACTCAAGT AAGAACCAGG CCAGCCTGAG ACTCAGCAGC 60

GTGACAGCCG CCGACACCGC 80

Pub. No. 97/000000

- 150 -

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GGTGTGCGCG GCTGTCACGC TGCTGAGTCT CAGGCTGGCC TGGTTCTTAC TTGAGTCTGC 60
CAGCATTGTG GCGC 74

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60
ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

- 151 -

CCTGGACGAG GCCTTGAGTG GATTGGATGG ATGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGCCACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

5 CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

10 (2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

25 Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
20 25 30

30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

35

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Arg Gly Arg Ala Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser
65 70 75 80

Downloaded from www.worldscientific.com

- 152 -

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys

85

90

95

5 His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Leu Val Thr Val Ser Ser

115

120

10

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

25

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

30 CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGCCACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGTCT ATTATTGTCA CGTCCTGATA 300

35

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

- 153 -

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn
 20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
 35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
 50 55 60

Arg Gly Arg Ala Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser
 65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

- 154 -

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

15
ATGAAGTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60
GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC GTACGGCCTA GCCAGACCCT GAGCCTCAG 120
20 TGCACCGCAT CTGGCTTCAA CATTAAAGGAC AATTACATGC ACTGGGTGAG ACAGCCACCT 180
GGACGAGGCC TTGAGTGGAT TGGATGGATT GACCCTGAGA ATGGTGACAC TGAGTACGCA 240
CCTAAGTTTC GCGGCCGCGT GACAATGCTG GCAGACACTA GTAAGAACCA GTTCAGCCTG 300
25
AGACTCAGCA GCGTGACAGC CGCCGACACC GCGGTCTATT ATTGTCACGT CCTGATATAC 360
GCCGGGTATC TGGCAATGGA CTACTGGGGC CAAGGGACCC TCGTCACCGT GAGCTCGGCC 420
30 TCCACCAAGG GCCCATCGGT CTTCCCCCTG GCACCCTCCT CCAAGAGCAC CTCTGGGGGC 480
ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540
AACTCAGGCG CCCTGACCAG CGGCGTGAC ACCTTCCCCG CTGTCCTACA GTCCTCAGGA 600
35
CTCTACTCCC TCAGCAGCGT GGTGACTGTG CCCTCCAGCA GCTTGGGCAC CCAGACCTAC 660
ATCTGCAACG TGAATCACA CCCCAGCAAC ACCAAGGTCG ACAAGAAAGT TGAGCCCCAA 720

- 155 -

TCTTGTGACA AGACGCACAC GTGCCC GCCG TGCCCGGCTC CGGAAGTCT GGGTGGCCCCG 780

5 (2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

20

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly
 1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg
 20 25 30

25

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
 35 40 45

30

Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
 50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala
 65 70 75 80

35

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn
 85 90 95

- 156 -

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 100 105 110

5 Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 130 135 140

10 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 165 170 175

15 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 20 195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 210 215 220

25 Asn His Asn Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
 245 250 255

30 Leu Gly Gly Pro
 260

(2) INFORMATION FOR SEQ ID NO: 94:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 base pairs

(B) TYPE: nucleic acid

- 157 -

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

10

ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60

GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC GTACGGCCTA GCCAGACCCT GAGCCTCAGC 120

15 TGCACCGCAT CTGGCTTCAA CATTAAAGGAC AATTACATGC ACTGGGTGAG ACAGCCACCT 180

GGACGAGGCC TTGAGTGGAT TGGATGGATT GACCCTGAGA ATGGTGACAC TGAGTACGCA 240

CCTAAGTTTC GCGGCCGCGT GACAATGCTG GCAGACACTA GTAAGAACCA GTTCAGCCTG 300

20

AGACTCAGCA GCGTGACAGC CGCCGACACC GCGGTCTATT ATTGTCACGT CCTGATATAC 360

GCCGGGTATC TGGCAATGGA CTACTGGGGC CAAGGGACCC TCGTCACCGT GAGCTCGGCT 420

25 AGCACCAAGG GCCCATCGGT CTTCCCCCTG GCGCCCTGCT CCAGGAGCAC CTCTGGGGGC 480

ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540

AACTCAGGCG CCCTGACCAG CGGCGTGAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA 600

30

CTCTACTCCC TCAGCAGCGT GGTGACCGTG CCCTCCAGCA GCTTGGGCAC CCAGACCTAC 660

ACCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAGAGT GGAGCTGAAA 720

35 ACCCCACTCG GTGACACAAC TCACACGTGC CCTAGGTGTC CTGAACCTAA ATCTTGTGAC 780

ACACCTCCCC CGTGCCCACG GTGCCCAGAG CCCAAATCTT GCGACACGCC CCCACCGTGT 840

PCT/GB97/01165

- 158 -

CCCAGATGTC CTGAACCAAA GAGCTGTGAC ACTCCACCGC CCTGCCCCGAG GTGCCCAGCA 900

CCTGAACTCC TGGGAGGG 918

5 (2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

20 Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly
1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg
20 25 30

25 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
35 40 45

30 Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala
65 70 75 80

35 Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn
85 90 95

- 159 -

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 100 105 110

5 Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr
 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 130 135 140

10 Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly
 145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 15 165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190

20 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val
 210 215 220

25 Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys
 225 230 235 240

Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro
 30 245 250 255

Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys
 260 265 270

35 Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser
 275 280 285

- 160 -

Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu
290 295 300

5 Gly Gly
305

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60
CGCGGCCAGA TCGTGCTGAC CCAGAGCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120
25 GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACCTACA TGCACTGGTA CCAGCAGAAG 180
CCAGGTAAGG CTCCAAAGCT GCTGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240
30 AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300
CCAGAGGATA TCGCCACCTA CTA CTGCCCAG CAGAGGAGTA CTTACCCGCT CACGTTCCGC 360
CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420
35 CCATCTGATG AGCAATTGAA ATCTGGAAGT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480
TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

- 161 -

CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCTG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

5

GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 97:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

25

Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ser Ser
20 25 30

30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
35 40 45

Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

35

Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

- 162 -

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile
 85 90 95

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg
 5 100 105 110

Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 10 130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 15 165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 20 180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 25 210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

30

(2) INFORMATION FOR SEQ ID NO: 98:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35

- 163 -

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

10 CGCGGCGACA TCCAGATGAC CCAGAGCCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120

GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACCTACA TGCACTGGTA CCAGCAGAAG 180

CCAGGTAAGG CTCCAAAGCT GTGGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240

15 AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300

CCAGAGGATA TCGCCACCTA CTA CTGCTGAGT CAGAGGAGTA CTTACCCGCT CAGGTTCCGC 360

20 CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

CCATCTGATG AGCAGTTGAA ATCTGGAAGT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

25 CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTTG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

30 GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 164 -

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

10 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
 20 25 30
 15 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
 35 40 45
 Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 50 55 60
 20 Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile
 25 85 90 95
 Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg
 100 105 110
 30 Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 115 120 125
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 130 135 140
 35 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 145 150 155 160

- 165 -

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

5 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

10 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

15 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: other nucleic acid

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CCCAGCACCT GAATCCTGG GAGGAGCAAC AGGACACAGT TATGAGAAGT ACAA

54

(2) INFORMATION FOR SEQ ID NO: 101:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

- 166 -

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

10 GGGGGTCTAG ATTATTAGTA CAGGTGTTCC AGGACGTAGC TGGCAACATA

50

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

25

GGGGGAGCTC GGCTAGCACC AAGGGCCCAT CGGTCTTCCC CCTGGC

46

(2) INFORMATION FOR SEQ ID NO: 103:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

- 167 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTGTACTTCT CATAACTGTG TCCTGTTGCT CCTCCCAGGA GTTCAGGTGC TGGGC

55

5 (2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

20 GCCTGTGCTC AATATTGATG G

21

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

- 168 -

GGAGAAAGCC ATATCTGCCT G

21

(2) INFORMATION FOR SEQ ID NO: 106:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TCGCTATTAC CATGGTGATG CGGTTTGGC

30

20 (2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: other nucleic acid

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GGCTGGATTC TCACTGGCGA CTT

23

35

(2) INFORMATION FOR SEQ ID NO: 108:

- 169 -

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

CACAACAGAG GCAGTTCC

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CACCTTCACC ATCAGCAGCC

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- 170 -

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

10 GGACCTGCTG CAGAGTCTG

19

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GGCTGCAGGA ATTCTTATTA TAGACGAACC CGGCTATCAA ACTGAGC

47

(2) INFORMATION FOR SEQ ID NO: 112:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1870 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- 171 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

AAGCTTGCCG CCACCATGAA GTTGTGGCTG AACTGGATTT TCCTTGTAAC ACTTTTAAAT 60

5 GGAATTCAGT GTGAGGTGCA GCTGCAGCAG AGCGGTCCAG GTCTCGTACG GCCTAGCCAG 120

ACCTGAGCC TCACGTGCAC CGCATCTGGC TTCAACATTA AGGACAATTA CATGCACTGG 180

GTGAGACAGC CACCTGGACG AGGCCTTGAG TGGATTGGAT GGATTGACCC TGAGAATGGT 240

10 GACACTGAGT ACGCACCTAA GTTTCGCGGC CGCGTGACAA TGCTGGCAGA CACTAGTAAG 300

AACCAGTTCA GCCTGAGACT CAGCAGCGTG ACAGCCGCCG ACACCGCGGT CTATTATTGT 360

15 CACGTCCTGA TATACGCCGG GSTATCTGGCA ATGGACTACT GGGGCCAAGG GACCCTCGTC 420

ACCGTGAGCT CGGCTAGCAC CAAGGGCCCA TCGGTCTTCC CCCTGGCGCC CTGCTCCAGG 480

AGCACCTCTG GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCC GAACCG 540

20 GTGACGGTGT CGTGGAATC AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC 600

CTACAGTCCT CAGGACTCTA CTCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG 660

25 GGCACCCAGA CCTACACCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGGACAAG 720

AGAGTGGAGC TGAAAACCCC ACTCGGTGAC ACAACTCACA CGTGCCCTAG GTGTCCTGAA 780

CCTAAATCTT GTGACACACC TCCCCGTGC CCACGGTGCC CAGAGCCCAA ATCTTGCGAC 840

30 ACGCCCCCAC CGTGTCCCAG ATGTCCTGAA CCAAAGAGCT GTGACACTCC ACCGCCCTGC 900

CCGAGGTGCC CAGCACCTGA ACTCCTGGGA GGAGCAACAG GACACAGTTA TGAGAAGTAC 960

35 AACAAAGTGG AAACGATAGA GGCTTGGA CTCAAGTCG CCACTGAGAA TCCAGCCCTC 1020

ATCTCTCGCA GTGTTATCGG AACCACATTT GAGGGACGCG CTATTTACCT CCTGAAGGTT 1080

- 172 -

GGCAAAGCTG GACAAAATAA GCCTGCCATT TTCATGGACT GTGGTTTCCA TGCCAGAGAG 1140

TGGATTTCTC CTGCATTCTG CCAGTGGTTT GTAAGAGAGG CTGTTTCGTAC CTATGGACGT 1200

5 GAGATCCAAG TGACAGAGCT TCTCGACAAG TTAGACTTTT ATGTCCTGCC TGTGCTCAAT 1260

ATTGATGGCT ACATCTACAC CTGGACCAAG AGCCGATTTT GGAGAAAGAC TCGCTCCACC 1320

CATACTGGAT CTAGCTGCAT TGGCACAGAC CCCAACAGAA ATTTTGATGC TGGTTGGTGT 1380

10 GAAATTGGAG CCTCTCGAAA CCCCTGTGAT GAAACTTACT GTGGACCTGC CGCAGAGTCT 1440

GAAAAGGAGA CCAAGGCCCT GGCTGATTTC ATCCGCAACA AACTCTCTTC CATCAAGGCA 1500

15 TATCTGACAA TCCACTCGTA CTCCCAAATG ATGATCTACC CTTACTCATA TGCTTACAAA 1560

CTCGGTGAGA ACAATGCTGA GTTGAATGCC CTGGCTAAAG CTACTGTGAA AGAACTTGCC 1620

TCACTGCACG GCACCAAGTA CACATATGGC CCGGGAGCTA CAACAATCTA TCCTTCTGCT 1680

20 GGGACTTCTA AAGACTGGGC TTATGACCAA GGAATCAGAT ATTCCTTCAC CTTTGAACCT 1740

CGAGATACAG GCAGATATGG CTTTCTCCTT CCAGAATCCC AGATCCGGGC TACCTGCGAG 1800

25 GAGACCTTCC TGGCAATCAA GTATGTTGCC AGCTACGTCC TGGAACACCT GTACTAATAA 1860

TCTAGAGAGA 1870.

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 613 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 173 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly

1 5 10 15

5

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg

20 25 30

10

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile

35 40 45

Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu

50 55 60

15

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala

65 70 75 80

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn

85 90 95

20

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val

100 105 110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr

25

115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly

130 135 140

30

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly

145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

165 170 175

35

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

180 185 190

- 174 -

	Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
	195 200 205
5	Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val
	210 215 220
	Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys
	225 230 235 240
10	Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro
	245 250 255
	Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys
	260 265 270
15	Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser
	275 280 285
	Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu
20	290 295 300
	Gly Gly Ala Thr Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr
	305 310 315 320
25	Ile Glu Ala Trp Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile
	325 330 335
	Ser Arg Ser Val Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu
	340 345 350
30	
	Leu Lys Val Gly Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp
	355 360 365
35	Cys Gly Phe His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp
	370 375 380

- 175 -

Phe Val Arg Glu Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr
 385 390 395 400

5 Glu Leu Leu Asp Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile
 405 410 415

Asp Gly Tyr Ile Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr
 420 425 430

10 Arg Ser Thr His Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg
 435 440 445

Asn Phe Asp Ala Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys
 450 455 460

15 Asp Glu Thr Tyr Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys
 465 470 475 480

20 Ala Leu Ala Asp Phe Ile Arg Asn Lys Leu Ser Ser Ile Lys Ala Tyr
 485 490 495

Leu Thr Ile His Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr
 500 505 510

25 Ala Tyr Lys Leu Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys
 515 520 525

Ala Thr Val Lys Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr
 530 535 540

30 Gly Pro Gly Ala Thr Thr Ile Tyr Pro Ser Ala Gly Thr Ser Lys Asp
 545 550 555 560

35 Trp Ala Tyr Asp Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg
 565 570 575

Asp Thr Gly Arg Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala
 580 585 590

- 176 -

Thr Cys Glu Glu Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val

595

600

605

5 Leu Glu His Leu Tyr

610

(2) INFORMATION FOR SEQ ID NO: 114:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

His His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn

1

5

10

15

25 Val Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr

20

25

30

Thr Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro

35

40

45

30

His Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val

50

55

60

Glu Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser

35

65

70

75

80

Asn Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Leu

85

90

95

- 177 -

(2) INFORMATION FOR SEQ ID NO: 115:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

- (ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

60 GAGCTCGGCT AGCACCAAGG GCCCATCGGT CTTCCCCCTG GCGCCCTGCT CCAGGAGCAC

20 CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC 120

GGTGTCTGG AACTCAGGCG CCCTGACCAG CGGCGTGAC ACCTTCCCGG CTGTCCTACA 180

GTCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG CCCTCCAGCA GCTTGGGCAC 240

25 CCAGACCTAC ACCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAGAGT 300

GGAGCTGAAA ACCCCACTCG GTGACACAAC TCACACGTGC CCTAGGTGTC CTGAACCTAA 360

30 ATCTTGTGAC ACACCTCCCC CGTGCCACG GTGCCAGAG CCCAAATCTT GCGACACGCC 420

CCCACCGTGT CCCAGATGTC CTGAACCAA GAGCTGTGAC ACTCCACCGC CCTGCCCCGAG 480

GTGCCAGCA CCTGAACTCC TGGGAGGGTA ATAGCCCGGG 520

35

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:

- 178 -

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GTTATTACTC GCTGCCCAAC CAGCCATGGC G

31

15 (2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

30 GCAGCAGGAT AGATTGTTGT AGC

23

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- 179 -

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

CCGGAATTCT TATTAGTTCA GGTCTCCTC AGAGATCAGC TTCTGCTCCT CGAACTCATG 60

10

GTGGTGATGG TGGTGGTACA GGTGTTCC 88

(2) INFORMATION FOR SEQ ID NO: 119:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CAATCTATCC TGCTGCTGGG ACTTCTAAAG 30

30 (2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- 180 -

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

GATTGTTGTA GCTCCCGGGC

20

10 (2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

25 GGAGCTACAA CAATCTATCC TTCTGCTGGG

30

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

35

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

- 181 -

ACGGCACCAA GTACACATAT GG

22

(2) INFORMATION FOR SEQ ID NO: 123:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ACGAGAATTC GACCGCTCTG CTGCAGCTGC ACCTCGGAAC CGCCACCGCT GCCACCGCCA 60

20 GAACCGCCAC CGTACAGGTG TTCCAGGACG 90

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 2154 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

35 ATGTTGGCAC TCTTGTTCT GGTGACTGTG GCCCTGGCAT CTGCTCATCA TGGTGGTGAG 60

CACTTTGAAG GCGAGAAGGT GTTCCGTGTT AACGTTGAAG ATGAAAATCA CATTACATA 120

- 182 -

ATCCGCGAGT TGGCCAGCAC GACCCAGATT GACTTCTGGA AGCCAGATTC TGTCACACAA 180

ATCAAACCTC ACAGTACAGT TGA CTTCCTGT GTTAAAGCAG AAGATACTGT CACTGTGGAG 240

5 AATGTTCTAA AGCAGAATGA ACTACAATAC AAGGTACTGA TAAGCAACCT GAGAAATGTG 300

GTGGAGGCTC AGTTTGATAG CCGGGTTCGT GCAACAGGAC ACAGTTATGA GAAGTACAAC 360

AAGTGGGAAA CGATAGAGGC TTGGACTCAA CAAGTCGCCA CTGAGAATCC AGCCCTCATC 420

10 TCTCGCAGTG TTATCGGAAC CACATTGAG GGACGCGCTA TTTACCTCCT GAAGGTTGGC 480

AAAGCTGGAC AAAATAAGCC TGCCATTTTC ATGGACTGTG GTTTCCATGC CAGAGAGTGG 540

15 ATTTCTCCTG CATTCGCGA GTGGTTTGTA AGAGAGGCTG TTCGTACCTA TGGACGTGAG 600

ATCCAAGTGA CAGAGCTTCT CGACAAGTTA GACTTTTATG TCCTGCCTGT GCTCAATATT 660

GATGGCTACA TCTACACCTG GACCAAGAGC CGATTTTGGA GAAAGACTCG CTCCACCCAT 720

20 ACTGGATCTA GCTGCATTGG CACAGACCCC AACAGAAATT TTGATGCTGG TTGGTGTGAA 780

ATTGGAGCCT CTCGAAACCC CTGTGATGAA ACTTACTGTG GACCTGCCGC AGAGTCTGAA 840

25 AAGGAGACCA AGGCCCTGGC TGATTTCATC CGCAACAAAC TCTCTTCCAT CAAGGCATAT 900

CTGACAATCC ACTCGTACTC CCAAATGATG ATCTACCCTT ACTCATATGC TTACAAACTC 960

GGTGAGAAC A TGCTGAGTT GAATGCCCTG GCTAAAGCTA CTGTGAAAGA ACTTGCCTCA 1020

30 CTGCACGGCA CCAAGTACAC ATATGGCCCG GGAGCTACAA CAATCTATCC TTCTGCTGGG 1080

ACTTCTAAAG ACTGGGCTTA TGACCAAGGA ATCAGATATT CCTTCACCTT TGA ACTTCGA 1140

35 GATACAGGCA GATATGGCTT TCTCCTTCCA GAATCCCAGA TCCGGGCTAC CTGCGAGGAG 1200

ACCTTCCTGG CAATCAAGTA TGTGCCAGC TACGTCCTGG AACACCTGTA CGGTGGCGGT 1260

- 183 -

TCTGGCGGTG GCAGCGGTGG CGGTTCCGAG GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC 1320
 GTACGGCCTA GCCAGACCCT GAGCCTCAGC TGCACCGCAT CTGGCTTCAA CATTAAGGAC 1380
 5 AATTACATGC ACTGGGTGAG ACAGCCACCT GGACGAGGCC TTGAGTGGAT TGGATGGATT 1440
 GACCCTGAGA ATGGTGACAC TGAGTACGCA CCTAAGTTTC GCGGCCGCGT GACAATGCTG 1500
 GCAGACACTA GTAAGAACCA GTTCAGCCTG AGACTCAGCA GCGTGACAGC CGCCGACACC 1560
 10 GCGGTCTATT ATTGTCACGT CCTGATATAC GCCGGGTATC TGGCAATGGA CTACTGGGGC 1620
 CAAGGGACCC TCGTCACCGT GAGCTCGGCT AGCACCAAGG GCCCATCGGT CTTCCCCCTG 1680
 15 GCGCCCTGCT CCAGGAGCAC CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GTTCAAGGAC 1740
 TACTTCCCCG AACCGGTGAC GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGAC 1800
 ACCTTCCCCG CTGTCCTACA GTCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG 1860
 20 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ACCTGCAACG TGAATCACA GCCCAGCAAC 1920
 ACCAAGGTGG ACAAGAGAGT GGAGCTGAAA ACCCCACTCG GTGACACAAC TCACACGTGC 1980
 25 CCTAGGTGTC CTGAACCTAA ATCTTGTGAC ACACCTCCCC CGTGCCCACG GTGCCCAGAG 2040
 CCCAAATCTT GCGACACGCC CCCACCGTGT CCCAGATGTC CTGAACCAAA GAGCTGTGAC 2100
 ACTCCACCGC CCGTCCCGAG GTGCCAGCA CCTGAACTCC TGGGAGGGTA ATAG 2154
 30

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 716 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 184 -

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Met Leu Ala Leu Leu Val Leu Val Thr Val Ala Leu Ala Ser Ala His

1 5 10 15

His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn Val

20 25 30

Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr Thr

35 40 45

Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro His

50 55 60

Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val Glu

65 70 75 80

Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser Asn

85 90 95

Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Ala Thr

100 105 110

Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr Ile Glu Ala Trp

115 120 125

Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile Ser Arg Ser Val

130 135 140

Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu Leu Lys Val Gly

145 150 155 160

- 185 -

Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp Cys Gly Phe His
 165 170 175

5 Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp Phe Val Arg Glu
 180 185 190

Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr Glu Leu Leu Asp
 195 200 205

10 Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile Asp Gly Tyr Ile
 210 215 220

15 Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr Arg Ser Thr His
 225 230 235 240

Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg Asn Phe Asp Ala
 245 250 255

20 Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys Asp Glu Thr Tyr
 260 265 270

Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys Ala Leu Ala Asp
 275 280 285

25 Phe Ile Arg Asn Lys Leu Ser Ser Ile Lys Ala Tyr Leu Thr Ile His
 290 295 300

Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr Ala Tyr Lys Leu
 305 310 315 320

30 Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys Ala Thr Val Lys
 325 330 335

35 Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr Gly Pro Gly Ala
 340 345 350

Thr Thr Ile Tyr Pro Ser Ala Gly Thr Ser Lys Asp Trp Ala Tyr Asp
 355 360 365

- 186 -

Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr Gly Arg
 370 375 380

5 Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala Thr Cys Glu Glu
 385 390 395 400

Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val Leu Glu His Leu
 405 410 415

10 Tyr Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln
 420 425 430

15 Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser
 435 440 445

Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn Tyr Met His
 450 455 460

20 Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly Trp Ile
 465 470 475 480

Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe Arg Gly Arg
 485 490 495

25 Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu
 500 505 510

30 Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys His Val Leu
 515 520 525

Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu
 530 535 540

35 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 545 550 555 560

- 187 -

Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 565 570 575

5 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 580 585 590

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 595 600 605

10 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 610 615 620

15 Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn
 625 630 635 640

Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr
 645 650 655

20 Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro
 660 665 670

Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro
 675 680 685

25 Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
 690 695 700

Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly
 705 710 715

30

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 188 -

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

TATATAAAGC TTGCCGCCAC CATGGGCCAC ACACGGAGGC AG

42

10 (2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

25 ACTCCACCAG CTTACCTCG TTATCAGGAA AATGCTCTTG CTTGG

45

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

- 189 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

AGAGCATTTT CCTGATAACG AGGTGAAGCT GGTGGAGTCT GGAGG

45

5

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

CCAGGCATCC CAGGGTCACC ATGGAGTTAG TTTGGGCAGC

40

20

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

30

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:16..1435

35

PCT/GB97/01165

- 190 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AAGCTTGCCG CCACC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 51
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser
 5 1 5 10

AAG TGT CCA TAC CTC AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT 99
 Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu
 15 20 25

10
 TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA 147
 Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu
 30 35 40

15 GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA 195
 Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala
 45 50 55 60

CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG 243
 20 Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met
 65 70 75

ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC 291
 Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile
 25 80 85 90

TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA 339
 Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro
 95 100 105

30
 TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC 387
 Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp
 110 115 120

35 GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT 435
 Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala
 125 130 135 140

- 191 -

GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT 483
 Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn
 145 150 155

5 ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC 531
 Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His
 160 165 170

CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA 579
 10 Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr
 175 180 185

GTT TCC CAA GAT CCT GAA ACT GAG CTC TAT GCT GTT AGC AGC AAA CTG 627
 Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu
 15 190 195 200

GAT TTC AAT ATG ACA ACC AAC CAC AGC TTC ATG TGT CTC ATC AAG TAT 675
 Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr
 205 210 215 220

20 GGA CAT TTA AGA GTG AAT CAG ACC TTC AAC TGG AAT ACA ACC AAG CAA 723
 Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln
 225 230 235

25 GAG CAT TTT CCT GAT AAC GAG GTG AAG CTG GTG GAG TCT GGA GGA GGC 771
 Glu His Phe Pro Asp Asn Glu Val Lys Leu Val Glu Ser Gly Gly Gly
 240 245 250

30 TTG GTA CAG CCT GGG GGT TCT CTG AGA CTC TCC TGT GCA ACT TCT GGG 819
 Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly
 255 260 265

TTC ACC TTC ACT GAT TAC TAC ATG AAC TGG GTC CGC CAG CCT CCA GGA 867
 35 Phe Thr Phe Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly
 270 275 280

AAG GCA CTT GAG TGG TTG GGT TTT ATT GGA AAC AAA GCT AAT GGT TAC 915

Lys Ala Leu Glu Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr
285 290 295 300

ACA ACA GAG TAC AGT GCA TCT GTG AAG GGT CGG TTC ACC ATC TCC AGA 963
5 Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
305 310 315

GAC AAA TCC CAA AGC ATC CTC TAT CTT CAA ATG AAC ACC CTG AGA GCT 1011
Asp Lys Ser Gln Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala
10 320 325 330

GAG GAC AGT GCC ACT TAT TAC TGT ACA AGA GAT AGG GGG CTA CGG TTC 1059
Glu Asp Ser Ala Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe
335 340 345

15

TAC TTT GAC TAC TGG GGC CAA GGC ACC ACT CTC ACA GTC TCC TCA GCC 1107

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala

350 355 360

20 AAA ACG ACA CCC CCA TCT GTC TAT CCA CTG GCC CCT GGA TCT GCT GCC 1155
Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala
365 370 375 380

CAA ACT AAC TCC ATG GTG ACC CTG GGA TGC CTG GTC AAG GGC TAT TTC 1203
25 Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe
385 390 395

CCT GAG CCA GTG ACA GTG ACC TGG AAC TCT GGA TCT CTG TCC AGC GGT 1251
Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly
30 400 405 410

GTG	CAC	ACC	TTC	CCA	GCT	GTC	CTG	CAG	TCT	GAC	CTC	TAC	ACT	CTG	AGC	1299
Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	
415				420				425								

35

AGC TCA GTG ACT GTC CCC TCC AGC ACC TGG CCC AGC GAG ACC GTC ACC 1347

Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr

430 435 440

- 193 -

TGC AAC GTT GCC CAC CCG GCC AGC AGC ACC AAG GTG GAC AAG AAA ATT 1395
 Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile
 445 450 455 460

5

GTG CCC AGG GAT TGT GGT TGT AAG CCT TGC ATA TGT ACA T AGTAAGAATT 1445
 Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr
 465 470

10 c

1446

(2) INFORMATION FOR SEQ ID NO: 131:

15

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1 5 10 15

25

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 20 25 30

30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 50 55 60

35

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 65 70 75 80

- 194 -

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
85 90 95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
5 100 105 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
115 120 125

10 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
130 135 140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
145 150 155 160

15 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
165 170 175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
20 180 185 190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
195 200 205

25 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
210 215 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
30 225 230 235 240

Asp Asn Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
245 250 255

35 Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr
260 265 270

Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu
275 280 285

Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr
-290 295 300

Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Gln
305 310 315 320

10 Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Ser Ala
325 330 335

Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr
340 345 350

15

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro

355 360 365

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
20 370 375 380

Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
385 390 395 400

25 Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
405 410 415

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
420 425 430

30
Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
435 440 445

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
35 450 455 460

Cys Gly Cys Lys Pro Cys Ile Cys Thr
465 470